



TITLE:

Resume : Estimating the number of HIV-infected individuals in Japan using a mathematical model (Theory of Biomathematics and Its Applications XI)

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Resume: Estimating the number of HIV-infected individuals in Japan using a mathematical model

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Resume of forthcoming article

As the original study is expected to be printed elsewhere, here we provide a Resume of our presented study for this report.

Background

Although the increase in the number of AIDS cases among Japanese had been considered slowing, the numbers of HIV and AIDS cases had continue to be the largest ever recorded in the last decade. The number of people with HIV/AIDS in Japan is still believed to continue to grow, and the previous underestimates might originate from the analyses based on invalid mathematical & statistical estimations.

Methods to reconstruct past HIV infection patterns and project AIDS incidence have been primarily based on backcalculation applied to AIDS incidence data using information on the incubation period distribution and model for the epidemic curve of HIV. Further, dynamic model of the AIDS epidemic has helped in understanding the essential components of the epidemic, in the evaluation of control measures and so forth. However, there are several sources of uncertainty in the fitted models and estimates based on them, including uncertainty about the form of the epidemic curves of HIV infection and distribution of the incubation period (i.e., the effect of antiretroviral therapy) and uncertainty about the substantial delays in diagnosis and reporting.

This study was aimed to develop the estimation method, which can reasonably resolve the problems in uncertainties, based on a multistate model using the number of AIDS diagnosis (without information of previous diagnosis) and HIV detection data.

Method

Basic model structure

We applied a three-stage multistate model to HIV/AIDS surveillance data. Movements towards the right represent disease progression. Movement downwards represents the diagnosis (first positive test). Similar models have been applied to different conditions of statistical records elsewhere.

Available data

HIV/AIDS surveillance record in Japan: Bimonthly (1984 -2000) or quarterly (2001-present) numbers of HIV infection and AIDS diagnosis are obtained. Among AIDS diagnosis, information with regard to previous HIV diagnosis is not available. Reporting interval in surveillance system is revised due to the different law (AIDS Prevention Law 1989-1999 and the National Epidemiological Surveillance of Infectious Diseases from Mar. 1999). Registration system of AIDS excluded those who were diagnosed as HIV-infected after the revision.

For simplicity, we assume the same diagnosis rates for different stages of infection. We obtained the maximum likelihood estimates of unknown parameters including the HIV incidence and the rate of diagnosis. Using covariance matrix and performing the simulations, we obtained the variation of the maximum likelihood estimates according to asymptotic theory. As in a parametric bootstrap, we used the resampled estimates to generate new predictions. This also enabled us to validate the uncertainties in the duration of incubation period.

Results

Estimated numbers of HIV-infected in each stage were obtained. Total number of individuals who are living with HIV/AIDS as of April 2014 was estimated as the order of 25000. Prediction of the total number of new AIDS diagnoses is presented in graphical form. Incidence of AIDS is still expected to increase in Japan. As a visual confirmation of the goodness-of-fit, observed and expected cumulative numbers of HIV infections and AIDS cases are also validated.

Discussion

Without previous information of HIV-diagnosis, we obtained estimates based on surveillance based records. 95%CI was derived from Bootstrap method. Although the total number is rather small compared to other industrialized countries, the number of HIV/AIDS in Japan is still steadily increasing. Our proposed method requires smaller amount of input data and less unrealistic assumptions as compared to existing models, and the model has been flexibly time inhomogeneous.

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